



Table III

Oligonucleotide Primers Used for RT-PCR Analysis and DNA Sequencing

Primer	SEQ ID NO:	Sequence	Position	PCR Product (bp)	Peptide Sequences confirmed
BAB1F	5	TCAATATAATCTGGCGAATGCAAT	3-26		
HSP2R	7	AGTTCCGAATGGGCAGGTCAGCTC	397-420	418	3
BAB3F	26	ATGAGGAAGCTCGGGTTAAAG	1452-1472		
BAB4R	29	GATGTAGCCATTGTTTGTGCCAA	1769-1792	341	2
HSP2F	33	GAGCTGACCTGCCCATTCGGAAC	397-420		
HSP3R	35	CTTTAACCCGAGCTTCCTCAT	1452-1472	1076	4
BAB6F	30	AGACGCCAAATGTGTGACCTCCA	3078-3101		
BAB7R	31	GAATAGGCCAGCACTTCCGTCAGG	3510-3533	456	2
BAB1F	5	TCAATATAATCTGGCGAATGCAAT	3-26		
BAB10R	32	GGTGAGGCAGTTGGCGCTGGTATG	851-874	872	3
HSP2F	33	GAGCTGACCTGCCCATTCGGAAC	397-420		
BAB10R	32	GGTGAGGCAGTTGGCGCTGGTATG	851-874	478	3
BAB10F	34	CATACCAGCGCCAACTGCCTCACC	851-874		
HSP3R	35	CTTTAACCCGAGCTTCCTCAT	1452-1472	622	3
BAB9F	36	CAAGTACGGCATCCACTGTGACCA	697-720		
HSP3R	35	CTTTAACCCGAGCTTCCTCAT	1452-1472	776	3

Other Primers used for RT-PCR and sequencing.

Name	SEQ ID NO:	Sequence	Position
5F	37	GGCTACTTCGGGCGAGACTGTCAG	2386-2409
5R	38	CTGACAGTCTCGCCCGAAGTAGCC	2386-2409
8F	39	TTGTACTCTTCAGCTGGCACC	4406-4426
8R	6	GGTGCCAGCTGAAGAGTACAA	4406-4426

Table IV

Summary of Amino Acid Sequences Derived From Peptides of the
Purified Human 190 kDa HARE Protein

The human HARE proteins were immuno-affinity-purified from human spleen, subjected to SDS-PAGE and the 190 kDa protein band was excised and analyzed for internal peptide sequence following trypsin digestion. The amino acid sequences of these ten tryptic peptides were highly homologous or identical to the sequences of the rat 175 kDa HARE, reported herein above, and seven of these (not in bold face) were identical to regions within a human hypothetical protein of unknown expression and unknown function under GenBank accession number BAB15793. HARE peptides in boldface were not in the ORF for BAB15793.

Peptide Designation	Amino Acid Sequences	Start-End Residue	SEQ ID NO:
PR 1822	XSKPK	758-761	40
PR 1823	LTFDK	1054-1058	41
PR 1825-1 st	GSIQELPK	440-448	42
PR 1825-2 nd	GTLFVPQNSGLGE	1198-1210	43
PR 1826	DLVGPGPFTVFAPLSAAFDEEAR	466-488	44
PR 1869-1st	ELTSPFGTK	133-141	45
PR 1869-2 nd	MPQVLR	498-503	46
PR 1870	SPLGQYK	1047-1053	47
PR 1871-1st	VLEIQK	107-112	48
PR 1872	VIHGLGK	100-106	49

Table V

Molecular Mass Mapping of Peptides Derived From the

Human 190 kDa HARE Protein

THE MOLECULAR MASSES OF SEVEN PEPTIDES DERIVED FROM TRYPTIC DIGESTION OF THE PURIFIED HUMAN 190 KDA HARE PROTEIN WERE DETERMINED BY MALDI-TOF MASS SPECTROMETRY AT THE LOUISIANA STATE UNIVERSITY PROTEIN CHEMISTRY FACILITY CORRESPONDED WITH PERFECT IDENTITY TO DEDUCED SEQUENCES WITHIN A PREDICTED HUMAN PROTEIN OF UNKNOWN FUNCTION (ACCESSION NUMBER BAB15793). THE MONOISOTOPIC PEPTIDE MASSES WERE SEARCHED AGAINST ENTRIES IN THE DATABASE, USING PEPTIDESEARCH SOFTWARE FROM THE EMBL PROTEIN AND PEPTIDE GROUP. IDENTICAL MASSES ARE ASSIGNED IN THIS SEARCH IF THE DIFFERENCE BETWEEN THE OBSERVED AND PREDICTED (CALCULATED) MASSES FOR A PEPTIDE IS < 0.2 DA. THE CORRESPONDING STARTING AND ENDING RESIDUES FOR EACH PEPTIDE WITHIN THE DEDUCED PROTEIN SEQUENCE IS SHOWN. THE N-TERMINAL R OR K RESIDUES IN PARENTHESES INDICATE THE DEDUCED RESIDUE IN THE PROTEIN AND CONFIRM THAT TRYPSIN DIGESTION OCCURRED ON THE C-TERMINAL SIDE OF THOSE AMINO ACIDS AS EXPECTED.

Measured Mass (Da)	Calculated Mass (Da)	Mass Difference (Da)	Start-End Residues	Sequence in Deduced Human	SEQ ID NO:
599.273	599.294	-0.021	796-800	(K)GYFGR	50
671.384	671.399	-0.015	656-660	(K)FHVIR	51
792.621	792.426	0.195	1047-1053	(R)SPLGQYK	52
1034.621	1034.552	0.068	440-448	(R)GSIYQELPK	53
1061.781	1061.584	0.196	677-686	(K)TLQGSELSVK	54
1624.051	1623.886	0.165	1047-1060	(R)SPLGQYKLTFDKAR	55
1092.771	1092.588	0.183	495-503	(K)YGLMPQVLR	56



In the Sequence Listing:

Please delete the Sequence Listing submitted on pages 139-207 of the Specification and substitute therefore the substitute Sequence Listing filed herewith under 37 CFR 1.825. The Sequence Listing filed with the application on April 25, 2001 did not contain a SEQ ID NO:37, and therefore the substitute Sequence Listing submitted herewith has been renumbered so that SEQ ID NOs:38-57 are now SEQ ID NOs:37-56. The Specification has been amended herein above to also reflect such renumbering of the SEQ ID NOs. In addition, the substitute Sequence Listing has been reformatted to fully comply with 37 CFR 1.821-1.823. The substitute Sequence Listing contains no new matter.

Also submitted herewith is a substitute copy of the Computer Readable Form of the substitute Sequence Listing under 37 CFR 1.825 which fully complies with the requirements of 37 CFR 1.821-1.824. The Computer Readable Form contains all previously submitted data with the above requested amendments incorporated therein. The copy of the Sequence Listing in Computer Readable Form is the same as the substitute copy of the Sequence Listing filed herewith.